C. Remarks

The claims are 1-6, with claims 1 and 2 being independent. The independent claims have been amended to better define the present invention. Support for this amendment may be found, inter alia, in the specification at paragraphs [0017] and [0025] - [0028]. No new matter has been added. Reconsideration of the present claims is expressly requested.

Claims 1-6 stand rejected under 35 U.S.C. § 102(b) as being allegedly anticipated by Mark Chee et al., "Accessing Generic Information with High-Density DNA Arrays," 274 Science 610-614 (1996) (Chee). This rejection is respectfully traversed.

Prior to addressing the merits of rejection, Applicants would like to briefly review some of the key features and advantages of the presently claimed invention. As recited in claim 1, the 1st to the nth image template patterns are prepared to show a relationship between positions of single-stranded nucleic acid probes on the probe array and their fluorescence properties when single-stranded nucleic acids that are completely complementary to the respective probes form double-stranded nucleic acids with the probes on the array. Specifically, fluorescence image template patterns with a one-to-one correspondence to all predicted nucleotide sequences (reference sequences) are prepared by hybridizing each labeled reference sequence with the probe array in which one probe complementary to the reference sequence is present. Then, a test sample is separately reacted with the above probe array and the resultant fluorescence image is compared with the image template patterns. When the hybridization pattern of the test sample corresponds to one of the template patterns, the sequence of the tested sample is that of the sequence

used for that template pattern. With respect to claim 2, the present invention utilizes plural template patterns of positive probe spots, with each template pattern being a positional pattern of probe spots where one probe and other probes differing from that first probe by i bases are immobilized respectively, wherein number i is determined experimentally as a sufficient fluorescent intensity threshold.

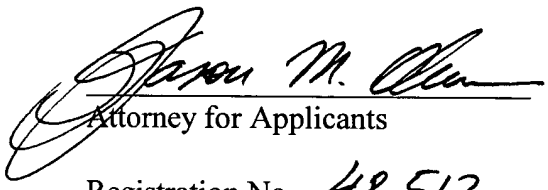
Thus, according to the present invention, a sequence of a test sample can be easily determined. The present invention also enables an easy and accurate sequence identification even when mutations are present at very close positions. Furthermore, the present invention enables sequence determination without analyzing fluorescence intensity at each spot.

Chee discloses that probes having one base mismatch to a certain reference sequence are located in a tilted array, and the pattern of fluorescent intensity obtained with the reference sequence is used as a template to compare with the fluorescent intensity pattern obtained with a target (see Fig. 2). Thus, Chee utilizes only one template pattern, which is clearly different from the present invention. Furthermore, Chee does not disclose or suggest utilizing plural template patterns of positive probe spots, with each template pattern being a positional pattern of probe spots where one probe and other probes differing from that first probe by i bases are immobilized respectively, wherein number i is determined experimentally as a sufficient fluorescent intensity threshold. Therefore, clearly, Chee cannot affect the patentability of the presently claimed invention.

Wherefore, it is respectfully requested that the outstanding rejection be withdrawn and the present case be passed to issue.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

Respectfully submitted,



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